What is claimed is:

1. A forensic method comprising the steps of:

determining a first molecular mass of a first amplification product of a first mitochondrial DNA identifying amplicon and comparing the first molecular mass to a second molecular mass of a second mitochondrial DNA identifying amplicon, wherein both first and second mitochondrial DNA identifying amplicons are correlative.

2. A forensic method of claim 1 wherein the second molecular mass of the second mitochondrial DNA identifying amplicon is indexed to a subject and contained in a database.

3. A forensic method of claim 2 wherein the subject is an animal.

4. A forensic method of claim 3 wherein the animal is a human.

5. A forensic method of claim 2 wherein the subject is a nonhuman eukaryotic organism, a fungus, a parasite, or a protozoan.

6. A forensic method of claim 1 wherein a first base composition signature is determined from the first molecular mass of the first amplification product and wherein the first base composition signature is compared to a second base composition signature determined for the second mitochondrial DNA identifying amplicon.

7. A forensic method of claim 6 wherein the second base composition signature is indexed to a subject and contained in a database.

8. A forensic method of claim 7 wherein the subject is an animal.

9. A forensic method of claim 8 wherein the animal is a human.

10. A forensic method of claim 7 wherein the subject is a nonhuman eukaryotic organism, a fungus, a parasite, or a protozoan.

11. A forensic method of claim 1 wherein the molecular mass of the amplification product is determined by ESI-FTICR mass spectrometry.

12. A forensic method of claim 1 wherein the molecular mass of the amplification product is determined by ESI-TOF mass spectrometry.

13. A forensic method of mitochondrial DNA analysis comprising the steps of:

digesting an amplification product of a first mitochondrial DNA identifying amplicon with restriction enzymes to produce a plurality of restriction fragments;

determining first molecular masses of the members of the plurality of restriction fragments; and

comparing the first molecular masses of the members of the plurality of restriction fragments with second molecular masses of restriction fragments of a second mitochondrial DNA identifying amplicon obtained with the restriction enzymes.

14. A forensic method of claim 13 wherein the second molecular masses of restriction fragments are indexed to a subject and contained in a database.

15. A forensic method of claim 13 wherein the restriction enzymes are any combination of RsaI , HpaII, HpyCH4IV, PacI, and EaeI.

16. A forensic method of claim 14 wherein the subject is an animal.

17. A forensic method of claim 16 wherein the animal is a human.

18. A forensic method of claim 14 wherein the subject is a nonhuman eukaryotic organism, a fungus, a parasite, or a protozoan.

19. A forensic method of claim 1 wherein the mitochondrial DNA identifying amplicon comprises a portion of a hypervariable region of mitochondrial DNA.

20. A forensic method of claim 19 wherein the hypervariable region comprises HV1 or HV2.

21. A forensic method for tracking the geographic location of a subject comprising the steps of:

determining a first molecular mass of a first amplification product of a first mitochondrial DNA identifying amplicon from a forensic sample containing mitochondrial DNA obtained from a geographic location;

comparing the first molecular mass to a second molecular mass of a second mitochondrial DNA identifying amplicon wherein both first and second mitochondrial DNA identifying amplicons are correlative, wherein a match between the first molecular mass and the second molecular mass indicates at least transient presence of the subject at the geographic location.

22. A method of characterizing the heteroplasmy of a sample of mitochondrial DNA comprising the steps of:

determining the molecular masses of a plurality of amplification products of the mitochondrial DNA; and

determining the relative quantities of the plurality of amplification products, thereby characterizing the heteroplasmy.

23. A method of claim 22 wherein a plurality of samples of mitochondrial DNA are obtained from an individual at different points of the lifetime of the individual, whereby the characterization of heteroplasmy indicates the rate of naturally occurring mutations in mitochondrial DNA.

24. A method of claim 23 further comprising correlating the rate of naturally occurring mutations in mitochondrial DNA with the rate of onset of mitochondrial disease in a plurality of individuals affected by mitochondrial disease, wherein the correlation provides a means for predicting the rate of onset of mitochondrial disease.

25. The method of claim 24 wherein the mitochondrial disease is Alpers Disease, Barth syndrome, Beta-oxidation Defects, Carnitine-Acyl-Carnitine Deficiency, Carnitine Deficiency , Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II Deficiency, Complex III Deficiency , Complex IV Deficiency, Complex V Deficiency, COX Deficiency, CPEO, CPT I Deficiency, CPT II Deficiency, Glutaric Aciduria Type II, KSS, Lactic

Acidosis, LCAD, LCHAD, Leigh Disease or Syndrome, LHON, Lethal Infantile Cardiomyopathy, Luft Disease, MAD, MCA, MELAS, MERRF, Mitochondrial Cytopathy, Mitochondrial DNA Depletion, Mitochondrial Encephalopathy, Mitochondrial Myopathy, MNGIE, NARP, Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase Deficiency, Respiratory Chain, SCAD, SCHAD, or VLCAD.

26. A primer having a nucleotide sequence comprising SEQ ID NO: 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, or 43.

27. The primer of claim 26 comprising at least one modified nucleobase.

28. The primer of claim 27 wherein said modified nucleobase is 5-propynyl-uridine or 5-propynyl-cytidine.